

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/208,629DATE: 12/10/2000  
TIME: 03:01:30

INPUT SET: S36189.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Coughlin, Shaun R.  
Ishihari, Hiroaki  
Connolly, Andrew

(ii) TITLE OF THE INVENTION: Protease-Activated Receptor  
3 and Uses Thereof

(iii) NUMBER OF SEQUENCES: 23 p. 3

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 755 Page Mill Road  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/208,629  
(B) FILING DATE: 08-DEC-1998  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/742,440  
(B) FILING DATE: 30-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Catherine M. Polizzi  
(B) REGISTRATION NUMBER: 40,130  
(C) REFERENCE/DOCKET NUMBER: 220002060310

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (650) 813-5600  
(B) TELEFAX: (650) 494-0792

Does Not Comply  
Corrected Diskette Needed

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47 (C) TELEX:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1224 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACATATTAA	GAGTTTAAAT	GGGGGTCCCC	180
AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
CTATAAAAGC	GGAGTGTCCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
CTTGCATGGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
CCTTAGCATT	CTTTGGGTTC	CTCATCCCGT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCCTCC	960
TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTACTT	TATGTATCTT	ATTGCTCTGT	1080
GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCCTTTA	CTTTGTCATG	TCGAAAGTTG	1140
TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
TCTGGGAAGA	CATACATGCT	TGGC				1224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA	ATATTTCTTT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
NNNTACAAC	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180

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100	CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTACCAG	CGAACATCGT	240
101	GACCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACACAA	300
102	CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCCG	TTTAAGATCN	NCCTACCATC	360
103	TCAATGGCAA	CAACTGGGTA	TTTGGCGAGG	TCATGTGCCG	GATCACCACG	GTCGTTTTCT	420
104	ACGGCAACAT	GTACTGCGCT	ANNNTCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
105	TGGCCACGGC	TCACCCTTTC	ACATAACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
106	TGTGTGGCAT	GGTGTGGGTC	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600
107	CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
108	GANTCCCAT	CATCCTTCCG	ATTCTACTAC	TTCGTCTCCT	TAGCATTCTT	TGGGTTCTCT	720
109	ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
110	GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCCTCA	TCCTTGTAAG	TTTACCACATC	840
111	TGCTTCCCCC	CCACCAAGNN	NNNNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
112	GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960
113	TTTGAGACAG	AGCCTCACTG	TGTAGTCCTG	GCTGGCCTGG	CTGGTTCTCT	ATTTAGACCA	1020
114	GGTTAGCCTT	GAACTCACAG	AGATCTGCCT	GCTTCTGCCT	CCCAAGTGCT	GGGTTCAACC	1080
115	AGGTCTGGCA	AGCGCTCCAT	TTTTCAGCTC	CTCTGCAACA	GTGC		1124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 5, 386, 394  
(D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Invalid Xaa

133	Thr	Leu	Tyr	Thr	Xaa	Gln	His	Pro	Val	Ala	Gly	Ser	Gln	Asp	Ile	Lys
134	1				5					10					15	
135	Met	Lys	Ile	Leu	Ile	Leu	Val	Ala	Ala	Gly	Leu	Leu	Phe	Leu	Pro	Val
136			20					25					30			
137	Thr	Val	Cys	Gln	Ser	Gly	Ile	Asn	Val	Ser	Asp	Asn	Ser	Ala	Lys	Pro
138			35				40					45				
139	Thr	Leu	Thr	Ile	Lys	Ser	Phe	Asn	Gly	Gly	Pro	Gln	Asn	Thr	Phe	Glu
140		50				55					60					
141	Glu	Phe	Pro	Leu	Ser	Asp	Ile	Glu	Gly	Trp	Thr	Gly	Ala	Thr	Thr	Thr
142	65				70					75				80		
143	Ile	Lys	Ala	Glu	Cys	Pro	Glu	Asp	Ser	Ile	Ser	Thr	Leu	His	Val	Asn
144				85					90				95			
145	Asn	Ala	Thr	Ile	Gly	Tyr	Leu	Arg	Ser	Ser	Leu	Ser	Thr	Gln	Val	Ile
146			100					105					110			
147	Pro	Ala	Ile	Tyr	Ile	Leu	Leu	Phe	Val	Val	Gly	Val	Pro	Ser	Asn	Ile
148			115				120					125				
149	Val	Thr	Leu	Trp	Lys	Leu	Ser	Leu	Arg	Thr	Lys	Ser	Ile	Ser	Leu	Val
150		130				135						140				
151	Ile	Phe	His	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Leu	Phe	Cys	Val	Thr	
152	145					150					155				160	

*This error appears in  
Seq. 6, too.*

*see p. 4, too*

*Xaa can only represent an  
amino acid. A group of  
4 or more amino acids*

*following a  
stop codon  
must  
be shown as  
a separate  
sequence,  
with a  
different  
sequence.*

*Identification  
number, and  
amino acids*

*also, the response for (iii) NUMBER OF SEQUENCES: must accommodate  
new sequences*

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153 Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe  
154 165 170 175  
155 Gly Glu Val Met Cys Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met  
156 180 185 190  
157 Tyr Cys Ala Ile Leu Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu  
158 195 200 205  
159 Ala Thr Ala His Pro Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe  
160 210 215 220  
161 Ser Leu Leu Met Cys Gly Ile Val Trp Val Met Val Phe Leu Tyr Met  
162 225 230 235 240  
163 Leu Pro Phe Val Ile Leu Lys Gln Glu Tyr His Leu Val His Ser Glu  
164 245 250 255  
165 Ile Thr Thr Cys His Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser  
166 260 265 270  
167 Phe Arg Phe Tyr Tyr Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile  
168 275 280 285  
169 Pro Phe Val Ile Ile Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu  
170 290 295 300  
171 Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu  
172 305 310 315 320  
173 Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu  
174 325 330 335  
175 Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr  
176 340 345 350  
177 Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu  
178 355 360 365  
179 Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn  
180 370 375 380  
181 Pro Xaa Ser Ala Met Ala Arg Pro Leu Xaa Arg Pro Arg Arg Asp Ile  
182 385 390 395 400  
183 Trp Glu Asp Ile His Ala Trp  
184 405  
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## (2) INFORMATION FOR SEQ ID NO:4:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

198	TGCTCCATGA	TTTTACAGAT	TTCATAACGT	TTAAGAGACG	GGACTCAGGT	CATCAAAATG	60
199	AAAGCCCTCA	TCTTTGCAGC	TGCTGGCCTC	CTGCTTCTGT	TGCCCACTTT	TTGTCAGAGT	120
200	GGCATGGAAA	ATGATACAAA	CAACTTGGCA	AAGCCAACCT	TACCCATTAA	GACCTTTCTG	180
201	GGAGCTCCCC	CAAATTCCTT	TGAAGAGTTC	CCCTTTTCTG	CCTTGGAAGG	CTGGACAGGA	240
202	GCCACGATTA	CTGTAAAAAT	TAAGTGCCCT	GAAGAAAGTG	CTTCACATCT	CCATGTGAAA	300
203	AATGCTACCA	TGGGGTACCT	GACCAGCTCC	TTAAGTACTA	AACTGATACC	TGCCATCTAC	360
204	CTCCTGGTGT	TTGTAGTTGG	TGTCCCGGCC	AATGCTGTGA	CCCTGTGGAT	GCTTTTCTTC	420
205	AGGACCAGAT	CCATCTGTAC	CACTGTATTC	TACACCAACC	TGGCCATTGC	AGATTTTCTT	480

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206	TTTTGTGTTA	CATTGCCCTT	TAAGATAGCT	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
207	GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
208	CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTCACCTAC	660
209	CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GACTGGTGTG	GGCAACAGTT	720
210	TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
211	ATCACCACCT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACCTCTAT	840
212	TACTTCATCT	CCTTGGCATT	CTTTGGATTG	TTAATTCCAT	TTGTGCTTAT	CATCTACTGC	900
213	TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTTAAG	960
214	GCGAGTCTCC	TCATCCTTGT	GATTTTTTACC	ATTTGCTTTG	CTCCAAGCAA	TATTATTCTT	1020
215	ATTATTCACC	ATGCTAACTA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
216	ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCCCTTA	TTTTCTCATG	1140
217	TCAAAAACCA	GAAATCACTC	CAGTGCTTAC	CTTACAAAAT	AGTGAAATGA	TCTTAGAGAA	1200
218	CAAGGACAGC	CATCACAGAG	AACG				1224

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

232	ACAGGCATGG	AAAATGATAC	AAACAACCTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
233	CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCTTTT	CTGCCTTGGA	AGGCTGGACA	120
234	GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
235	AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
236	TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAAATGCTG	TGACCCTGTG	GATGCTTTTC	300
237	TTCAGGACCA	GATCCATCTG	TACCACATGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
238	CTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
239	TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCATCTTCT	ATGGCAACAT	GTA CTGCTCC	480
240	ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTCACC	540
241	TACCGGGGCC	TGCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
242	GTTTTCTTAT	ATATGCTGCC	ATTTTTTATA	CTGAAGCAGG	AATATTATCT	TGTTTCAGCCA	660
243	GACATCACCA	CCTGCCATGA	TGTTTACAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACCTC	720
244	TATTACTTCA	TCTCCTTGGC	ATTCCTTTGGA	TTCTTAATTC	CATTGTGTGCT	TATCATCTAC	780
245	TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
246	AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTTGCT	TTGCTCCAAG	CAATATTATT	900
247	CTTATTATT	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
248	CTCATAGCTT	TGTGCCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTTCCT	TTATTTTCTC	1020
249	ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
250	GAACAAGGAC	AGCCATCACA	GA				1102

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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**SEQUENCE VERIFICATION REPORT**  
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